



PCT09

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/831,758A

DATE: 06/04/2002  
TIME: 16:03:52

Input Set : A:\46355862.app  
Output Set: N:\CRF3\06042002\I831758A.raw

3 <110> APPLICANT: WATANABE, TAKUYA  
 4 KIKUCHI, KUNIKO  
 5 TERAO, YASUKO  
 6 SHINTANI, YASUSHI  
 7 HINUMA, SHUJI  
 8 FUKUSUMI, SHOJI  
 9 FUJII, RYO  
 10 HOSOYA, MASAKI  
 11 KITADA, CHIEKO  
 13 <120> TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR PROTEIN, ITS DNA AND  
 14 LIGAND THEREOF  
 16 <130> FILE REFERENCE: 46342-55862  
 18 <140> CURRENT APPLICATION NUMBER: 09/831,758A  
 C--> 19 <141> CURRENT FILING DATE: 2002-04-05  
 21 <150> PRIOR APPLICATION NUMBER: JP 10-323759  
 22 <151> PRIOR FILING DATE: 1998-11-13  
 24 <150> PRIOR APPLICATION NUMBER: JP 11-0600030  
 25 <151> PRIOR FILING DATE: 1999-03-08  
 27 <150> PRIOR APPLICATION NUMBER: JP 11-106812  
 28 <151> PRIOR FILING DATE: 1999-04-14  
 30 <150> PRIOR APPLICATION NUMBER: JP 11-166672  
 31 <151> PRIOR FILING DATE: 1999-06-14  
 33 <150> PRIOR APPLICATION NUMBER: JP 11-221640  
 34 <151> PRIOR FILING DATE: 1999-08-04  
 36 <150> PRIOR APPLICATION NUMBER: JP 11-259818  
 37 <151> PRIOR FILING DATE: 1999-09-14  
 39 <160> NUMBER OF SEQ ID NOS: 63  
 41 <170> SOFTWARE: PatentIn Ver. 2.1  
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 44 <211> LENGTH: 180  
 45 <212> TYPE: PRT  
 46 <213> ORGANISM: Homo sapiens  
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 50 1 5 10 15  
 52 Ser Ser Leu Leu Thr Ser Asn Ile Phe Cys Ala Asp Glu Leu Val Met  
 53 20 25 30  
 55 Ser Asn Leu His Ser Lys Glu Asn Tyr Asp Lys Tyr Ser Glu Pro Arg  
 56 35 40 45  
 58 Gly Tyr Pro Lys Gly Glu Arg Ser Leu Asn Phe Glu Glu Leu Lys Asp  
 59 50 55 60  
 61 Trp Gly Pro Lys Asn Val Ile Lys Met Ser Thr Pro Ala Val Asn Lys  
 62 65 70 75 80

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64 Met Pro His Ser Phe Ala Asn Leu Pro Leu Arg Phe Gly Arg Asn Val  
65 85 90 95  
67 Gln Glu Glu Arg Ser Ala Gly Ala Thr Ala Asn Leu Pro Leu Arg Ser  
68 100 105 110  
70 Gly Arg Asn Met Glu Val Ser Leu Val Arg Arg Val Pro Asn Leu Pro  
71 115 120 125  
73 Gln Arg Phe Gly Arg Thr Thr Ala Lys Ser Val Cys Arg Met Leu  
74 130 135 140  
76 Ser Asp Leu Cys Gln Gly Ser Met His Ser Pro Cys Ala Asn Asp Leu  
77 145 150 155 160  
79 Phe Tyr Ser Met Thr Cys Gln His Gln Glu Ile Gln Asn Pro Asp Gln  
80 165 170 175  
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83 180  
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89 <213> ORGANISM: Homo sapiens  
91 <220> FEATURE:  
92 <221> NAME/KEY: CDS  
93 <222> LOCATION: (1)..(540)  
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98 1 5 10 15  
100 tca agc ttg tta aca tca aac att ttt tgt gca gat gaa tta gtg atg 96  
101 Ser Ser Leu Leu Thr Ser Asn Ile Phe Cys Ala Asp Glu Leu Val Met  
102 20 25 30  
104 tcc aat ctt cac agc aaa gaa aat tat gac aaa tat tct gag cct aga 144  
105 Ser Asn Leu His Ser Lys Glu Asn Tyr Asp Lys Tyr Ser Glu Pro Arg  
106 35 40 45  
108 gga tac cca aaa ggg gaa aga agc ctc aat ttt gag gaa tta aaa gat 192  
109 Gly Tyr Pro Lys Gly Glu Arg Ser Leu Asn Phe Glu Glu Leu Lys Asp  
110 50 55 60  
112 tgg gga cca aaa aat gtt att aag atg agt aca cct gca gtc aat aaa 240  
113 Trp Gly Pro Lys Asn Val Ile Lys Met Ser Thr Pro Ala Val Asn Lys  
114 65 70 75 80  
116 atg cca cac tcc ttc gcc aac ttg cca ttg aga ttt ggg agg aac gtt 288  
117 Met Pro His Ser Phe Ala Asn Leu Pro Leu Arg Phe Gly Arg Asn Val  
118 85 90 95  
120 caa gaa gaa aga agt gct gga gca aca gcc aac ctg cct ctg aga tct 336  
121 Gln Glu Glu Arg Ser Ala Gly Ala Thr Ala Asn Leu Pro Leu Arg Ser  
122 100 105 110  
124 gga aga aat atg gag gtg agc ctc gtg aga cgt gtt cct aac ctg ccc 384  
125 Gly Arg Asn Met Glu Val Ser Leu Val Arg Arg Val Pro Asn Leu Pro  
126 115 120 125  
128 caa agg ttt ggg aga aca aca aca gcc aaa agt gtc tgc agg atg ctg 432  
129 Gln Arg Phe Gly Arg Thr Thr Ala Lys Ser Val Cys Arg Met Leu  
130 130 135 140

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132	agt gat ttg tgt caa gga tcc atg cat tca cca tgt gcc aat gac tta	480
133	Ser Asp Leu Cys Gln Gly Ser Met His Ser Pro Cys Ala Asn Asp Leu	
134	145 150 155 160	
136	ttt tac tcc atg acc tgc cag cac caa gaa atc cag aat ccc gat caa	528
137	Phe Tyr Ser Met Thr Cys Gln His Gln Glu Ile Gln Asn Pro Asp Gln	
138	165 170 175	
140	aaa cag tca agg taa	543
141	Lys Gln Ser Arg	
142	180	
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148	<213> ORGANISM: Artificial Sequence	
150	<220> FEATURE:	
151	<223> OTHER INFORMATION: Description of Artificial Sequence: Primer	
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154	gggctgcaca tagagactta attttag	27
157	<210> SEQ ID NO: 4	
158	<211> LENGTH: 27	
159	<212> TYPE: DNA	
160	<213> ORGANISM: Artificial Sequence	
162	<220> FEATURE:	
163	<223> OTHER INFORMATION: Description of Artificial Sequence: Primer	
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166	ctagaccacc tctatataac tgcccat	27
169	<210> SEQ ID NO: 5	
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171	<212> TYPE: DNA	
172	<213> ORGANISM: Artificial Sequence	
174	<220> FEATURE:	
175	<223> OTHER INFORMATION: Description of Artificial Sequence: Primer	
177	<400> SEQUENCE: 5	
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181	<210> SEQ ID NO: 6	
182	<211> LENGTH: 27	
183	<212> TYPE: DNA	
184	<213> ORGANISM: Artificial Sequence	
186	<220> FEATURE:	
187	<223> OTHER INFORMATION: Description of Artificial Sequence: Primer	
189	<400> SEQUENCE: 6	
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195	<212> TYPE: DNA	
196	<213> ORGANISM: Artificial Sequence	
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199	<223> OTHER INFORMATION: Description of Artificial Sequence: Primer	
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Input Set : A:\46355862.app

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205 <210> SEQ ID NO: 8  
 206 <211> LENGTH: 196  
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 208 <213> ORGANISM: Homo sapiens  
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 212 1 5 10 15  
 214 Ser Ser Leu Leu Thr Ser Asn Ile Phe Cys Ala Asp Glu Leu Val Met  
 215 20 25 30  
 217 Ser Asn Leu His Ser Lys Glu Asn Tyr Asp Lys Tyr Ser Glu Pro Arg  
 218 35 40 45  
 220 Gly Tyr Pro Lys Gly Glu Arg Ser Leu Asn Phe Glu Glu Leu Lys Asp  
 221 50 55 60  
 223 Trp Gly Pro Lys Asn Val Ile Lys Met Ser Thr Pro Ala Val Asn Lys  
 224 65 70 75 80  
 226 Met Pro His Ser Phe Ala Asn Leu Pro Leu Arg Phe Gly Arg Asn Val  
 227 85 90 95  
 229 Gln Glu Glu Arg Ser Ala Gly Ala Thr Ala Asn Leu Pro Leu Arg Ser  
 230 100 105 110  
 232 Gly Arg Asn Met Glu Val Ser Leu Val Arg Arg Val Pro Asn Leu Pro  
 233 115 120 125  
 235 Gln Arg Phe Gly Arg Thr Thr Ala Lys Ser Val Cys Arg Met Leu  
 236 130 135 140  
 238 Ser Asp Leu Cys Gln Gly Ser Met His Ser Pro Cys Ala Asn Asp Leu  
 239 145 150 155 160  
 241 Phe Tyr Ser Met Thr Cys Gln His Gln Glu Ile Gln Asn Pro Asp Gln  
 242 165 170 175  
 244 Lys Gln Ser Arg Arg Leu Leu Phe Lys Lys Ile Asp Asp Ala Glu Leu  
 245 180 185 190  
 247 Lys Gln Glu Lys  
 248 195  
 251 <210> SEQ ID NO: 9  
 252 <211> LENGTH: 591  
 253 <212> TYPE: DNA  
 254 <213> ORGANISM: Homo sapiens  
 256 <220> FEATURE:  
 257 <221> NAME/KEY: CDS  
 258 <222> LOCATION: (1)..(588)  
 260 <400> SEQUENCE: 9

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 262 Met Glu Ile Ile Ser Ser Lys Leu Phe Ile Leu Leu Thr Leu Ala Thr  
 263 1 5 10 15  
 265 tca agc ttg tta aca tca aac att ttt tgt gca gat gaa tta gtg atg 96  
 266 Ser Ser Leu Leu Thr Ser Asn Ile Phe Cys Ala Asp Glu Leu Val Met  
 267 20 25 30  
 269 tcc aat ctt cac agc aaa gaa aat tat gac aaa tat tct gag cct aga 144  
 270 Ser Asn Leu His Ser Lys Glu Asn Tyr Asp Lys Tyr Ser Glu Pro Arg  
 271 35 40 45  
 273 gga tac cca aaa ggg gaa aga agc ctc aat ttt gag gaa tta aaa gat 192

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Input Set : A:\46355862.app  
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274	Gly	Tyr	Pro	Lys	Gly	Glu	Arg	Ser	Leu	Asn	Phe	Glu	Glu	Leu	Lys	Asp	
275	50				55				60								
277	tgg	gga	cca	aaa	aat	gtt	att	aag	atg	agt	aca	cct	gca	gtc	aat	aaa	240
278	Trp	Gly	Pro	Lys	Asn	Val	Ile	Lys	Met	Ser	Thr	Pro	Ala	Val	Asn	Lys	
279	65				70				75							80	
281	atg	cca	cac	tcc	ttc	gcc	aac	ttg	cca	ttg	aga	ttt	ggg	agg	aac	gtt	288
282	Met	Pro	His	Ser	Phe	Ala	Asn	Leu	Pro	Leu	Arg	Phe	Gly	Arg	Asn	Val	
283					85				90						95		
285	caa	gaa	gaa	aga	agt	gct	gga	gca	aca	gcc	aac	ctg	cct	ctg	aga	tct	336
286	Gln	Glu	Glu	Arg	Ser	Ala	Gly	Ala	Thr	Ala	Asn	Leu	Pro	Leu	Arg	Ser	
287					100				105						110		
289	gga	aga	aat	atg	gag	gtg	agc	ctc	gtg	aga	cgt	gtt	cct	aac	ctg	ccc	384
290	Gly	Arg	Asn	Met	Glu	Val	Ser	Leu	Val	Arg	Arg	Val	Pro	Asn	Leu	Pro	
291					115				120						125		
293	caa	agg	ttt	ggg	aga	aca	aca	aca	gcc	aaa	agt	gtc	tgc	agg	atg	ctg	432
294	Gln	Arg	Phe	Gly	Arg	Thr	Thr	Thr	Ala	Lys	Ser	Val	Cys	Arg	Met	Leu	
295					130				135						140		
297	agt	gat	ttg	tgt	caa	gga	tcc	atg	cat	tca	cca	tgt	gcc	aat	gac	tta	480
298	Ser	Asp	Leu	Cys	Gln	Gly	Ser	Met	His	Ser	Pro	Cys	Ala	Asn	Asp	Leu	
299	145				150				155						160		
301	ttt	tac	tcc	atg	acc	tgc	cag	cac	caa	gaa	atc	cag	aat	ccc	gat	caa	528
302	Phe	Tyr	Ser	Met	Thr	Cys	Gln	His	Gln	Glu	Ile	Gln	Asn	Pro	Asp	Gln	
303					165				170						175		
305	aaa	cag	tca	agg	aga	ctg	cta	ttc	aag	aaa	ata	gat	gat	gca	gaa	ttg	576
306	Lys	Gln	Ser	Arg	Arg	Leu	Leu	Phe	Lys	Lys	Ile	Asp	Asp	Ala	Glu	Leu	
307					180				185						190		
309	aaa	caa	gaa	aaa	taa												
310	Lys	Gln	Glu	Lys												591	
311		195															
314	<210>	SEQ ID NO:	10														
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316	<212>	TYPE:	DNA														
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320	<223>	OTHER INFORMATION:	Description of Artificial Sequence:	Primer													
322	<400>	SEQUENCE:	10														
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326	<210>	SEQ ID NO:	11														
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338	<210>	SEQ ID NO:	12														
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RAW SEQUENCE LISTING ERROR SUMMARY  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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Seq#:21; N Pos. 3,9,12  
Seq#:22; N Pos. 3,6,9  
Seq#:23; N Pos. 3,6,9,12  
Seq#:24; N Pos. 3,6,9  
Seq#:25; N Pos. 3,6,9,12